e.g., as set forth herein, can be developed and practiced. Certain quality control modules and links, as well as most of the generic artificial neural network learning components are omitted for clarity, but will be apparent to one of skill. The charts are in a continuous arrangement, each connectable head-to tail. Additional material and implementation of individual GO modules, and many arrangements of GOs in working sequences and trees, as used in GAGGS, are available in various software packages. Suitable references describing exemplar existing software are found, e.g., at aic.nrl.navy.mil/galist/ (on the world wide web) and at cs.purdue.edu/coast/archive/clife/FAQ/www/Q20_2.htm (on the world wide web). It will be apparent that many of the decision steps represented in Figs. 1-4 are performed most easily with the assistance of a computer, using one or more software program to facilitate selection/ decision processes.

In accordance with 37 CFR §1.121 a marked up version of the above-amended paragraph(s) illustrating the changes introduced by the forgoing amendment(s) are provided in Appendix C.

In the Claims:

Please amend the claims by substituting the following claims for the corresponding previously pending claims of the same number(s):

1 (AMENDED). A method of making a recombinant nucleic acid, the method comprising:

providing a plurality of parental character strings corresponding to a plurality of parental nucleic acids or to a plurality of parental polypeptides, which character strings, when aligned for maximum identity, comprise at least one region of heterology;

aligning the character strings;

defining a set of character string subsequences, which set of subsequences comprises a plurality of subsequences of each of at least two of the plurality of parental character strings;

providing a set of oligonucleotides corresponding to the set of character string subsequences,

annealing the set of oligonucleotides to each other; and,

elongating one or more members of the set of oligonucleotides with a polymerase, or ligating at least two members of the set of oligonucleotides with a ligase, thereby producing one or more recombinant nucleic acid.

2 (AMENDED). The method of claim 1, wherein the character strings, when aligned for maximum identity, comprise at least one region of similarity.

4 (AMENDED). The method of claim 1, wherein at least one of the parental character strings corresponds to a designed nucleic acid or designed polypeptide.

6 (AMENDED). The method of claim 1, further comprising applying one or more genetic operator to one or more of the parental character strings, or to one or more of the character string subsequences, wherein the genetic operator is selected from the group consisting of: a mutation of the one or more parental character strings or one or more character string subsequences, a multiplication of the one or more parental character strings or one or more character string subsequences, a fragmentation of the one or more parental character strings or one or more character string subsequences, a crossover between any of the one or more parental character strings or one or more character string subsequences or an additional character string, a ligation of the one or more parental character strings or one or more character string subsequences, an elitism calculation, a calculation of sequence homology or sequence similarity of aligned strings, a recursive use of one or more genetic operator for evolution of character strings, application of a randomness operator to the one or more parental character strings or the one or more character string subsequences, a deletion mutation of the one or more parental character strings or one or more character string subsequences, an insertion mutation into the one or more parental character strings or one or more of character string subsequences, subtraction of the of the one or more parental character strings or one or more character string subsequences with an inactive sequence, selection of the of the one or more parental character strings or one or more character string subsequences with an active sequence, and death of the one or more parental character strings or one or more of character string subsequences.

7 (AMENDED). The method of claim 1, further comprising generating a diplomat sequence, which diplomat sequence comprises an intermediate level of sequence similarity between

two or more additional members of the plurality of parental character strings wherein the set of oligonucleotides comprises or encodes subsequences of the diplomat sequence.

8 (AMENDED). The method of claim 1, further comprising selecting one or more cross-over sites between the two or more parental character strings and providing the set of oligonucleotides to comprise one or more bridging oligonucleotides.

9 (AMENDED). The method of claim 8, wherein the two or more parental character strings display low sequence similarity.

10 (TWICE AMENDED). The method of claim 8, further comprising determining a sequence for one or more putative recombinant nucleic acid or polypeptide resulting from in silico recombination of the two or more parental character strings at the cross-over sites, and performing one or more in silico simulation of activity for one or more of the putative recombinant nucleic acid or polypeptide.

17 (AMENDED). The method of claim 16, further comprising denaturing the extended double stranded nucleic acids, thereby producing a heterogeneous mixture of single-stranded nucleic acids.

21. (AMENDED). The method of claim 1, wherein the set of oligonucleotides is provided by synthesizing the oligonucleotides to comprise one or more modified parental character string subsequence, which subsequence comprises one or more of:

a parental character string subsequence modified by one or more replacement of one or more character of the parental character string subsequence with one or more different character;

a parental character string subsequence modified by one or more deletion or insertion of one or more characters of the parental character string subsequence;

a parental character string subsequence modified by inclusion of a degenerate sequence character at one or more randomly or non-randomly selected positions;

a parental character string subsequence modified by inclusion of a character string from a different character string from a second parental character string subsequence at one or more position;

a parental character string subsequence which is biased based upon its frequency in a selected library of nucleic acids; and,

a parental character string subsequence which comprises, or encodes a polypeptide that comprises, one or more sequence motif, which sequence motif is artificially included in the subsequence.

25. (AMENDED). The method of claim 1, wherein the plurality of parental character strings comprises at least two parental character strings, wherein the oligonucleotide set comprises at least one oligonucleotide member comprising a chimeric nucleic acid sequence that comprises a subsequence from each of at least two parental character strings, wherein the subsequences from each parental character string are separated by a crossover point.

26. (AMENDED). The method of claim 25, wherein the crossover point is selected by aligning at least one substring of each of at least two of the parental character strings to display pairwise identity between the substrings, and selecting a point within the aligned sequence as the crossover point.

34. (AMENDED). The method of claim 1, further comprising denaturing the recombinant nucleic acid, and contacting the recombinant nucleic acid with at least one additional nucleic acid produced by cleavage of at least one parental nucleic acid.

35. (AMENDED). The method of claim 1, further comprising denaturing the recombinant nucleic acid, and contacting the recombinant nucleic acid with at least one additional nucleic acid produced by cleavage of a parental nucleic acid, which parental nucleic acid is cleaved by one or more of: chemical cleavage, cleavage with a DNAse, and cleavage with a restriction endonuclease.

36. (AMENDED). The method of claim 1, wherein at least one parental nucleic acid encodes a protein selected from: erythropoietin (EPO), insulin, a peptide hormone, a cytokine, epidermal growth factor, fibroblast growth factor, hepatocyte growth factor, insulin-like growth factor, an interferon, an interleukin, a keratinocyte growth factor, a leukemia inhibitory factor, oncostatin M, platelet derived erythroid colony stimulating factor (PD-ECSF), Platelet-derived growth factor (PDGF), pleiotropin, stem cell factor (SCF), c-kit ligand, vascular endothelial growth factor (VEGF), granulocyte-colony stimulating factor (G-CSF), an oncogene product, a tumor suppressor, a steroid hormone receptor, a plant hormone, a disease resistance gene, an herbicide resistance gene product, a bacterial gene product, a monooxygenase, a protease, a nuclease, and a lipase.

38 (AMENDED). The method of claim 1, further comprising selecting the recombinant nucleic acid, or a polypeptide encoded by the recombinant nucleic acid for a desired trait or property, thereby providing a selected recombinant nucleic acid.

39 (AMENDED). The method of claim 38, further comprising recombining the selected recombinant nucleic acid with one or more of: a homolgous nucleic acid, or an oligonucleotide member from the set of oligonucleotides.

40 (AMENDED). The method of claim 1, further comprising selecting the recombinant nucleic acid for a desired trait or property, thereby providing a selected recombinant nucleic acid, wherein the desired trait or property is selected for in an in vivo selection assay or a parallel solid phase assay.

41 (AMENDED). The method of claim 1, further comprising selecting the recombinant nucleic acid for a desired trait or property, thereby providing a selected recombinant nucleic acid, wherein the desired trait or property is selected for in an in vitro selection assay.

46 (AMENDED). The method of claim 1, wherein the parental character strings, or oligonucleotide sets are provided in a computer.

47-92 are withdrawn

93. (AMENDED). A method of producing one or more recombinant nucleic acids, the method comprising:

providing initial character strings which represent two or more parental nucleic acids or parental polypeptides;

selecting cross-over sites for recombination between the initial character strings, thereby defining recombinant character strings that result from a cross-over between the character strings;

selecting a sequence of at least one of the recombinant character strings in silico for one or more expected activity of one or more corresponding recombinant nucleic acids or recombinant polypeptides; and,

synthesizing the one or more recombinant nucleic acids or recombinant polypeptides corresponding to one or more of the selected recombinant character strings.

94 (AMENDED). The method of claim 93, further comprising providing bridging oligonucleotides which correspond to the cross-over sites.

95. (TWICE AMENDED). The method of claim 94, wherein synthesizing the recombinant nucleic acid comprises providing fragments of two or more of the parental nucleic acids and at least one of the corresponding bridge oligonucleotides, hybridizing the fragments and the bridge oligonucleotides and elongating the hybridized fragments with a polymerase or a ligase.

96. (TWICE AMENDED). The method of claim 93, wherein the [sequences of the two or more parental nucleic acids] initial character strings display low sequence similarity.

97. (AMENDED). The method of claim 93, wherein selecting the sequence of at least one of the recombinant character strings in silico comprises one or more of:

(i) performing an energy minimization analysis of a protein encoded by the recombinant character strings;

(ii) performing a stability analysis of at least one protein encoded by the recombinant character strings;

(iii) comparing an energy minimized model of at least one protein encoded by the recombinant character strings to an energy minimized model of a protein encoded by the initial character strings;

(iv) performing protein threading on one or more protein encoded by the recombinant character strings, or the initial character strings; and,

(v) selecting the cross-over sites for recombination between the initial character strings to occur within regions of structural overlap of the parental nucleic acids or polypeptides;

(vi) performing one or more of: PDA, a branch-and-terminate combinatorial optimization analysis, a dead end elimination, a genetic or mean-field analysis, or an analysis of protein folding by threading, of the recombinant character strings or of a nucleic acid or polypeptide represented by the recombinant character strings;

(vii) performing PDA of at least one initial character string which represents the parental polypeptide or a protein encoded by at least one of the parental nucleic acids; or

(vii) comparing a PDA model of a protein encoded by the recombinant character strings to a PDA model of the parental polypeptide or a protein encoded by at least one of the two or more parental nucleic acids.

98 (AMENDED). The method of claim 93, wherein the step of selecting cross-over sites for recombination between the initial character strings and the step of selecting the at least one recombinant character string in silico are performed simultaneously.

PLEASE ENTER THE FOLLOWING NEW CLAIMS

99. The method of claim 1, wherein one or more of the parental character strings comprises a diplomat sequence.

100. The method of claim 8, wherein the two or more parental sequences are less than 50% similar.

101. The method of claim 93, wherein the two or more parental sequences are less than 50% similar.

These amendments are made without prejudice and are not to be construed as abandonment of the previously claimed subject matter or agreement with any objection or rejection